Claims:

1. In a method for improving the expression of a heterologous gene in plants by modifying the structural coding sequence of said gene, the improvement which comprises reducing the occurrence of polyadenylation signals selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

2. The method of Claim 1 further comprising the improvement of reducing the occurrence of ATTTA sequences within the structural coding sequence.

3. A method for modifying a wild-type structural gene sequence which encodes an insecticidal protein of *Bacillus thuringiensis* to enhance the expression of said protein in plants which comprises:

a) removing polyadenylation signals contained in said wild-type gene while retaining a sequence which encodes said protein; and

b) removing ATTTA sequences contained in said wild-type gene while retaining a sequence which encodes said protein.

4. A method of Claim 3 further comprising the removal of self-complementary sequences and replacement of such sequences with nonself-complementary DNA comprising plant preferred codons while retaining a structural gene sequence encoding said protein.

5. A method of Claim 4 further comprising the use of plant preferred sequences in the removal of the polyadenylation signals and ATTTA sequences.

6. A method of Claim 3 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

7. A method of Claim 4 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

8. A method of Claim 5 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

9. A method for modifying a wild-type structural gene sequence which encodes an insecticidal protein of *Bacillus thuringiensis* to enhance the expression of said protein in plants which comprises:

a) identifying regions within said sequence with greater than four consecutive adenine or thymine nucleotides;

b) modifying the regions of step (a) which have two or more polyadenylation signals within a ten base sequence to remove said signals while maintaining a gene sequence which encodes said protein; and

c) modifying the 15-30 base regions surrounding the regions of step (a) to remove major plant polyadenylation signals, consecutive sequences containing more than one minor polyadenylation

signal and consecutive sequences containing more than one ATTTA sequence while maintaining a gene sequence which encodes said protein.

10. A method of Claim 9 in which the major plant polyadenylation signals are selected from the group consisting of AATAAA and AATAAT.

11. A method of Claim 10 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

12. A method of Claim 11 further comprising the use of plant preferred sequences in the removal of polyadenylation signals and ATTTA sequences.

13. A structural gene which encodes an insecticidal protein of Bacillus thuringiensis, said gene being substantially devoid of polyadenylation signals and ATTTA sequences.

14. A structural gene of Claim 13 which is substantially devoid of polyadenylation signals selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

15. A structural gene of Claim 13 which encodes an insecticidal protein of *B.t.k.* HD-1 having the sequence:

```
                .         .         .         .
   1  ATGGCTATAGAAACTGGTTACACCCCAATCGATATTTCCT   40
                .         .         .         .
  41  TGTCGCTAACGCAATTTCTTTTGAGTGAATTTGTTCCCGG   80
                .         .         .         .
  81  TGCTGGATTTGTGTTAGGACTAGTTGATATTATCTGGGGA  120
                .         .         .         .
 121  ATTTTTGGTCCCTCTCAATGGGACGCATTTCTTGTACAAA  160
                .         .         .         .
 161  TTGAACAGCTCATCAACCAGAGAATCGAAGAGTTCGCTAG  200
                .         .         .         .
 201  GAATCAAGCCATTTCTAGATTAGAAGGACTAAGCAATCTT  240
                .         .         .         .
 241  TATCAAATTTACGCAGAATCTTTTAGAGAGTGGGAAGCAG  280
                .         .         .         .
 281  ATCCTACTAATCCAGCATTAAGAGAAGAGATGCGTATTCA  320
                .         .         .         .
 321  ATTCAATGACATGAACAGTGCCCTTACAACCGCTATTCCT  360
                .         .         .         .
 361  CTTTTTGCAGTTCAAAATTATCAAGTTCCTCTCCTCTCCG  400
                .         .         .         .
 401  TGTACGTTCAAGCTGCCAACCTCCACCTCTCAGTTTTGAG  440
                .         .         .         .
 441  AGATGTTTCAGTGTTTGGACAAAGGTGGGGATTTGATGCC  480
                .         .         .         .
 481  GCGACTATCAATAGTCGTTATAATGATTTAACTAGGCTTA  520
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521  TTGGCAACTATACAGATCATGCTGTACGCTGGTACAATAC  560
561  GGGATTAGAGCGTGTATGGGGACCGGATTCTAGAGATTGG  600
601  ATCAGGTACAACCAGTTCAGAAGAGAGCTTACACTAACTG  640
641  TATTAGATATCGTTTCTCTATTTCCGAACTATGATAGTAG  680
681  AACGTATCCAATTCGAACAGTTTCCCAATTAACAAGAGAA  720
721  ATTTATACAAACCCAGTATTAGAAAATTTTGATGGTAGTT  760
761  TTCGAGGCTCGGCTCAGGGCATAGAAGGAAGTATTAGGAG  800
801  TCCACATTTGATGGATATACTTAATAGTATAACCATCTAT  840
841  ACGGATGCTCATAGAGGAGAATACTACTGGTCCGGTCACC  880
881  AGATCATGGCTTCTCCTGTAGGGTTTTCGGGGCCAGAATT  920
921  CACTTTTCCGCTATATGGAACTATGGGAAATGCAGCTCCA  960
961  CAACAACGTATTGTTGCTCAACTAGGTCAGGGCGTGTATA  1000
1001 GAACATTATCGTCCACCTTATATAGAAGACCTTTTAACAT  1040
1041 CGGGATCAACAACCAACAACTATCTGTTCTTGACGGGACA  1080
1081 GAATTTGCTTATGGAACCTCCTCAAATTTGCCATCCGCTG  1120
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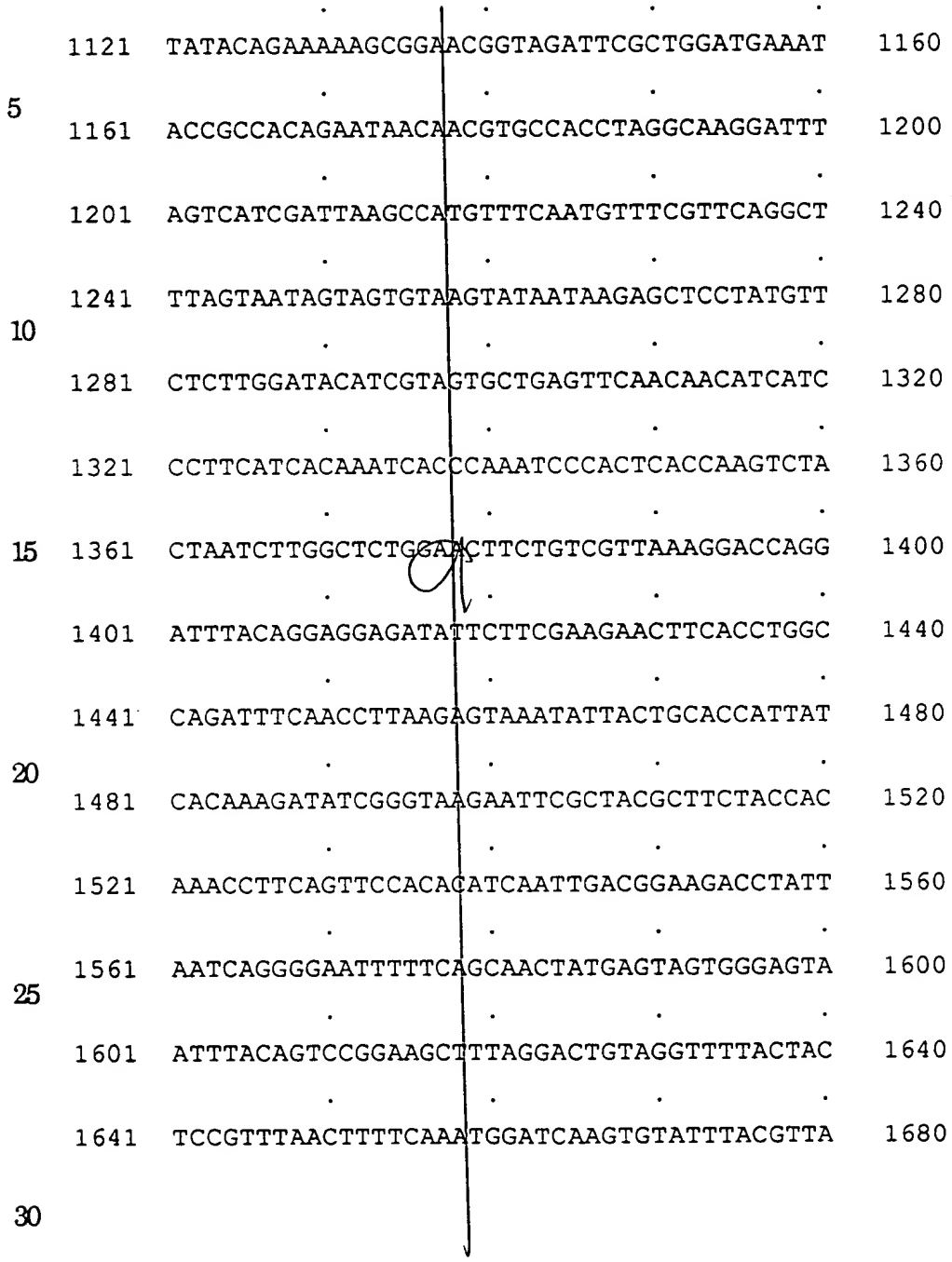
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1201 AGTCATCGATTAAGCCATGTTTCAATGTTTCGTTCAGGCT 1240
1241 TTAGTAATAGTAGTGTAAGTATAATAAGAGCTCCTATGTT 1280
1281 CTCTTGGATACATCGTAGTGCTGAGTTCAACAACATCATC 1320
1321 CCTTCATCACAAATCACCCAAATCCCACTCACCAAGTCTA 1360
1361 CTAATCTTGGCTCTGGAACTTCTGTCGTTAAAGGACCAGG 1400
1401 ATTTACAGGAGGAGATATTCTTCGAAGAACTTCACCTGGC 1440
1441 CAGATTTCAACCTTAAGAGTAAATATTACTGCACCATTAT 1480
1481 CACAAAGATATCGGGTAAGAATTCGCTACGCTTCTACCAC 1520
1521 AAACCTTCAGTTCCACACATCAATTGACGGAAGACCTATT 1560
1561 AATCAGGGGAATTTTTCAGCAACTATGAGTAGTGGGAGTA 1600
1601 ATTTACAGTCCGGAAGCTTTAGGACTGTAGGTTTTACTAC 1640
1641 TCCGTTTAACTTTTCAAATGGATCAAGTGTATTTACGTTA 1680

1681 AGTGCTCATGTCTTCAATTCAGGCAATGAAGTTTATATAG 1720

1721 ATCGAATTGAATTTGTTCCGGCA 1743.

16. A structural gene of Claim 13 which encodes an insecticidal protein of *B.t.k.* HD-73 having the sequence:

1 ATGGCCATTGAAACCGGTTACACTCCCATCGACATCTCCT 40

41 TGTCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGG 80

81 TGCTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGT 120

121 ATCTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAA 160

161 TTGAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAG 200

201 GAACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTC 240

241 TACCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCG 280

281 ATCCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCA 320

321 ATTCAACGACATGAACAGCGCCTTGACCACAGCTATCCCA 360

361 TTGTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCG 400

401 TGTACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCG 440

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441  AGACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCT  480
481  GCAACCATCAATAGCCGTTACAACGACCTTACTAGGCTGA  520
521  TTGGAAACTACACCGACCACGCTGTTCGTTGGTACAACAC  560
561  TGGCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGG  600
601  ATTAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAG  640
641  TTTTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAG  680
681  AACCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAA  720
721  ATCTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCT  760
761  TCCGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAG  800
801  CCCACACTTGATGGACATCTTGAACAGCATAACTATCTAC  840
841  ACCGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACC  880
881  AGATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTT  920
921  TACCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCA  960
961  CAACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACA  1000
1001 GAACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATAT  1040
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1041  CGGTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACA  1080
1081  GAGTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTG  1120
1121  TTTACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAAT  1160
1161  CCCACCACAGAACAACAATGTGCCACCCAGGCAAGGATTC  1200
1201  TCCCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGAT  1240
1241  TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTT  1280
1281  CTCTTGGATACACCGTAGTGCTGAGTTCAACAACATCATC  1320
1321  GCATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAA  1360
1361  ACTTTCTCTTCAACGGTTCTGTCATTTCAGGACCAGGATT  1400
1401  CACTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAAT  1440
1441  AACATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACT  1480
1481  TCCCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTA  1520
1521  TGCTTCTGTGACCCCTATTCACCTCAACGTTAATTGGGGT  1560
1561  AATTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTA  1600
1601  CCTCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTT  1640
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1641  TGAAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATC  1680

1681  GTGGGTGTTAGAAACTTTAGTGGGACTGCAGGAGTGATTA  1720

1721  TCGACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGA  1760

1761  GGCTGAG  1767.
```

17. A structural gene of Claim 13 encoding a insecticidal protein of *B.t.k.* HD-1 having the sequence:

```
   1  ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA   40

  41  ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA   80

  81  ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG  120

 121  TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG  160

 161  CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT  200

 201  CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT  240

 241  GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA  280

 281  ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA  320

 321  CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT  360
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361  CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT  400
401  TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT  440
441  GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG  480
481  TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG  520
521  ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCTGC  560
561  AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT  600
601  GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG  640
641  GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT  680
681  TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT  720
721  TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA  760
761  CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT  800
801  CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC  840
841  CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC  880
881  CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC  920
921  CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG  960
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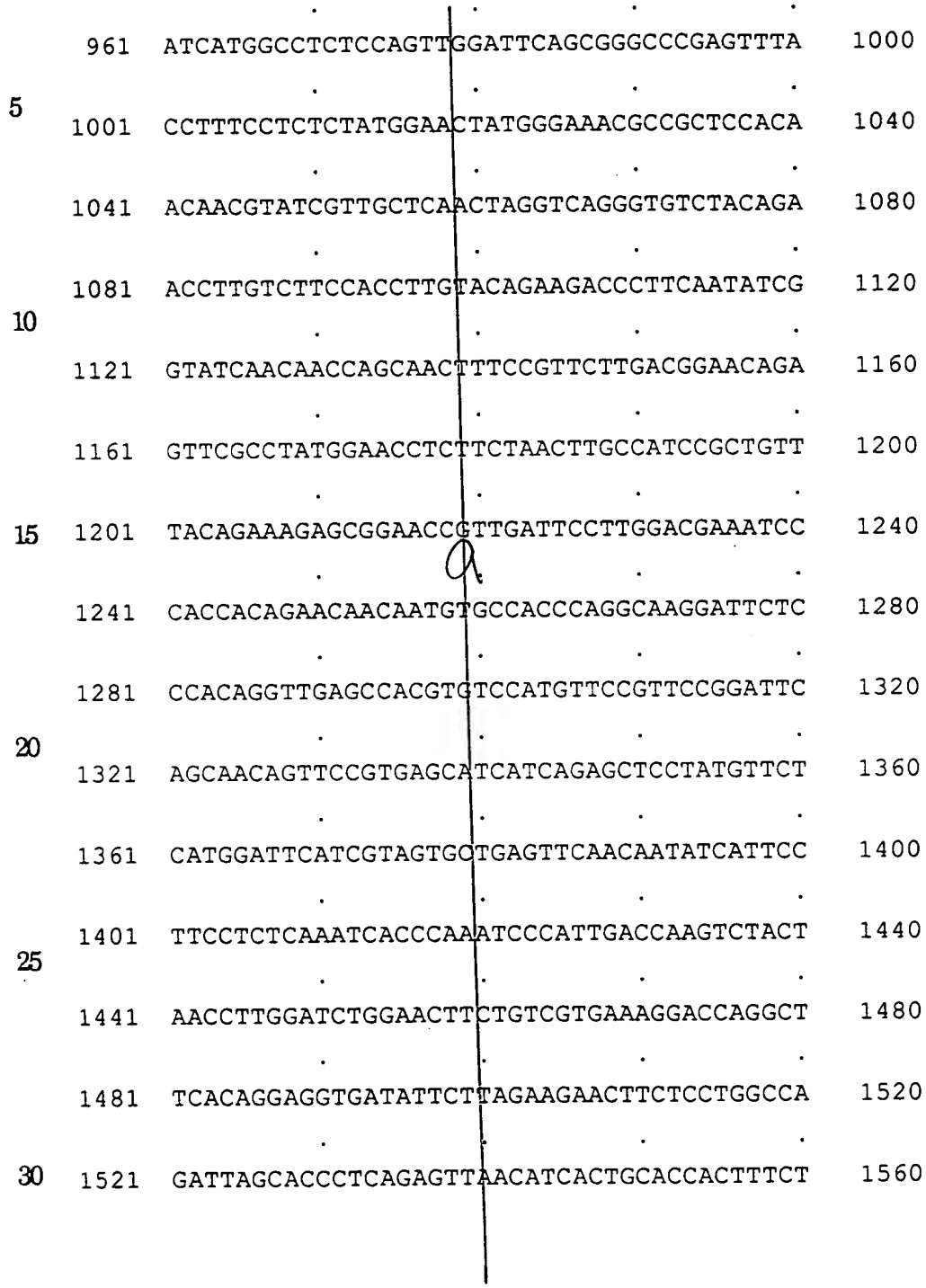
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1001 CCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCACA 1040
1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA 1080
1081 ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG 1120
1121 GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA 1160
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT 1200
1201 TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC 1240
1241 CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC 1280
1281 CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC 1320
1321 AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT 1360
1361 CATGGATTCATCGTAGTGCTGAGTTCAACAATATCATTCC 1400
1401 TTCCTCTCAAATCACCCAAATCCCATTGACCAAGTCTACT 1440
1441 AACCTTGGATCTGGAACTTCTGTCGTGAAAGGACCAGGCT 1480
1481 TCACAGGAGGTGATATTCTTAGAAGAACTTCTCCTGGCCA 1520
1521 GATTAGCACCCTCAGAGTTAACATCACTGCACCACTTTCT 1560

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1561  CAAAGATATCGTGTCAGGATTCGTTACGCATCTACCACTA  1600
1601  ACTTGCAATTCCACACCTCCATCGACGGAAGGCCTATCAA  1640
1641  TCAGGGTAACTTCTCCGCAACCATGTCAAGCGGCAGCAAC  1680
1681  TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTC  1720
1721  CTTTCAACTTCTCTAACGGATCAAGCGTTTTCACCCTTAG  1760
1761  CGCTCATGTGTTCAATTCTGGCAATGAAGTGTACATTGAC  1800
1801  CGTATTGAGTTTGTGCCTGCCGAAGTTACCTTCGAGGCTG  1840
1841  AGTAC  1845.
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18. A structural gene of Claim 13 encoding an insecticidal protein derived from *B.t.*k. HD-73 having the sequence:

```
   1  ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA   40
  41  ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA   80
  81  ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG  120
 121  TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG  160
 161  CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT  200
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201  CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT  240
241  GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA  280
281  ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA  320
321  CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT  360
361  CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT  400
401  TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT  440
441  GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG  480
481  TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG  520
521  ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCTGC  560
561  AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT  600
601  GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG  640
641  GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT  680
681  TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT  720
721  TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA  760
761  CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT  800
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801  CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC  840
841  CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC  880
881  CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC  920
921  CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG  960
961  ATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTTTA  1000
1001 CCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCACA  1040
1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA  1080
1081 ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG  1120
1121 GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA  1160
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT  1200
1201 TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC  1240
1241 CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC  1280
1281 CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC  1320
1321 AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT  1360
1361 CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC  1400
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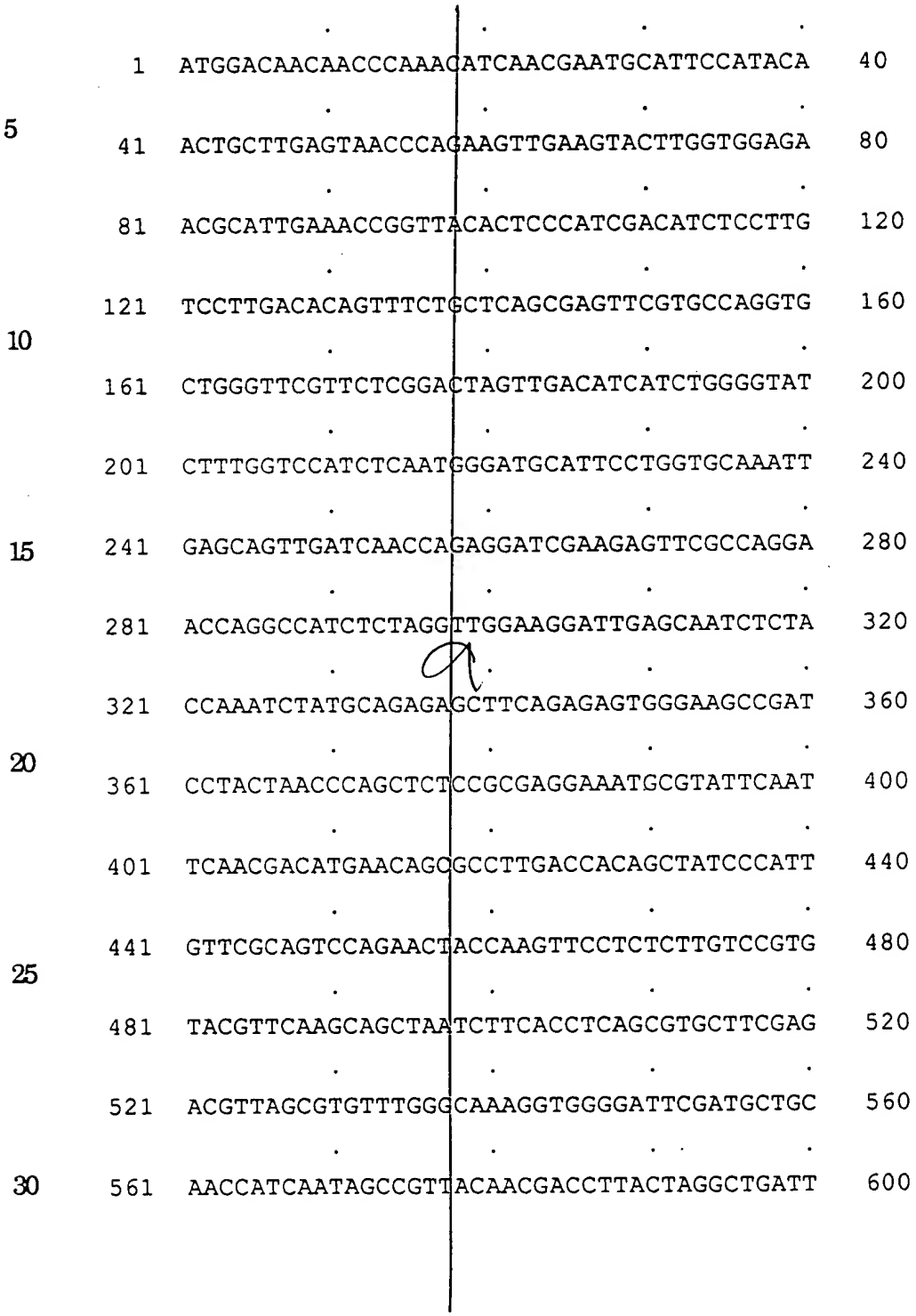
1401  ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC  1440
1441  TTTCTCTTCAACGGTTCTGTCATTTCAGGACCAGGATTCA  1480
1481  CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA  1520
1521  CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTC  1560
1561  CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG  1600
1601  CTTCTGTGACCCCTATTCACCTCAACGTTAATTGGGGTAA  1640
1641  TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC  1680
1681  TCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTTTG  1720
1721  AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT  1760
1761  GGGTGTTAGAAACTTTAGTGGGACTGCAGGAGTGATTATC  1800
1801  GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG  1840
1841  CTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTAATGCG  1880
1881  CTGTTTACGTCTACAAACCAGCTTGGACTCAAGACAAATG  1920.
```

19. A structural gene of Claim 13 encoding the full-length insecticidal protein of *B.t.k.* HD-73 having the sequence: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41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA 80
81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG 120
121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160
161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200
201 CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT 240
241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280
281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA 320
321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT 360
361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT 400
401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT 440
441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG 480
481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG 520
521 ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCTGC 560
561 AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT 600

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601  GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG  640
641  GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT  680
681  TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT  720
721  TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA  760
761  CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT  800
801  CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC  840
841  CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC  880
881  CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC  920
921  CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG  960
961  ATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTTTA  1000
1001 CCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCACA  1040
1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA  1080
1081 ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG  1120
1121 GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA  1160
1161 GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT  1200
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1201  TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC  1240
1241  CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC  1280
1281  CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC  1320
1321  AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT  1360
1361  CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC  1400
1401  ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC  1440
1441  TTTCTCTTCAACGGTTCTGTCATTTCAGGACCAGGATTCA  1480
1481  CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA  1520
1521  CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTC  1560
1561  CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG  1600
1601  CTTCTGTGACCCCTATTCACCTCAACGTTAATTGGGGTAA  1640
1641  TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC  1680
1681  TCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTTTG  1720
1721  AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT  1760
1761  GGGTGTTAGAAACTTTAGTGGGACTGCAGGAGTGATTATC  1800
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1801  GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG  1840
1841  CTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTGAATGC  1880
1881  GCTGTTTACGTCTACAAACCAGCTCGGCCTCAAGACCAAT  1920
1921  GTGACGGATTATCATATTGATCAAGTGTCCAACTTGGTGA  1960
1961  CCTACCTCAGCGATGAGTTCTGTCTGGATGAAAAGCGAGA  2000
2001  ATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGAT  2040
2041  GAACGCAATTTACTCCAAGATTCAAATTTCAAAGACATTA  2080
2081  ATAGGCAACCAGAACGTGGGTGGGGCGGAAGTACAGGGAT  2120
2121  TACCATCCAGGGAGGTGACGACGTGTTCAAGGAGAACTAC  2160
2161  GTCACACTATCAGGTACCTTTGATGAGTGCTATCCAACAT  2200
2201  ACCTCTACCAGAAGATCGACGAGTCCAAGTTGAAAGCCTT  2240
2241  TACCCGTTATCAATTAAGAGGGTATATCGAAGATAGTCAA  2280
2281  GACCTCGAGATCTACCTCATCCGCTACAATGCAAAACATG  2320
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2361  TTCAGCCCAAAGTCCAATCGGAAAGTGTGGAGAGCCGAAT  2400
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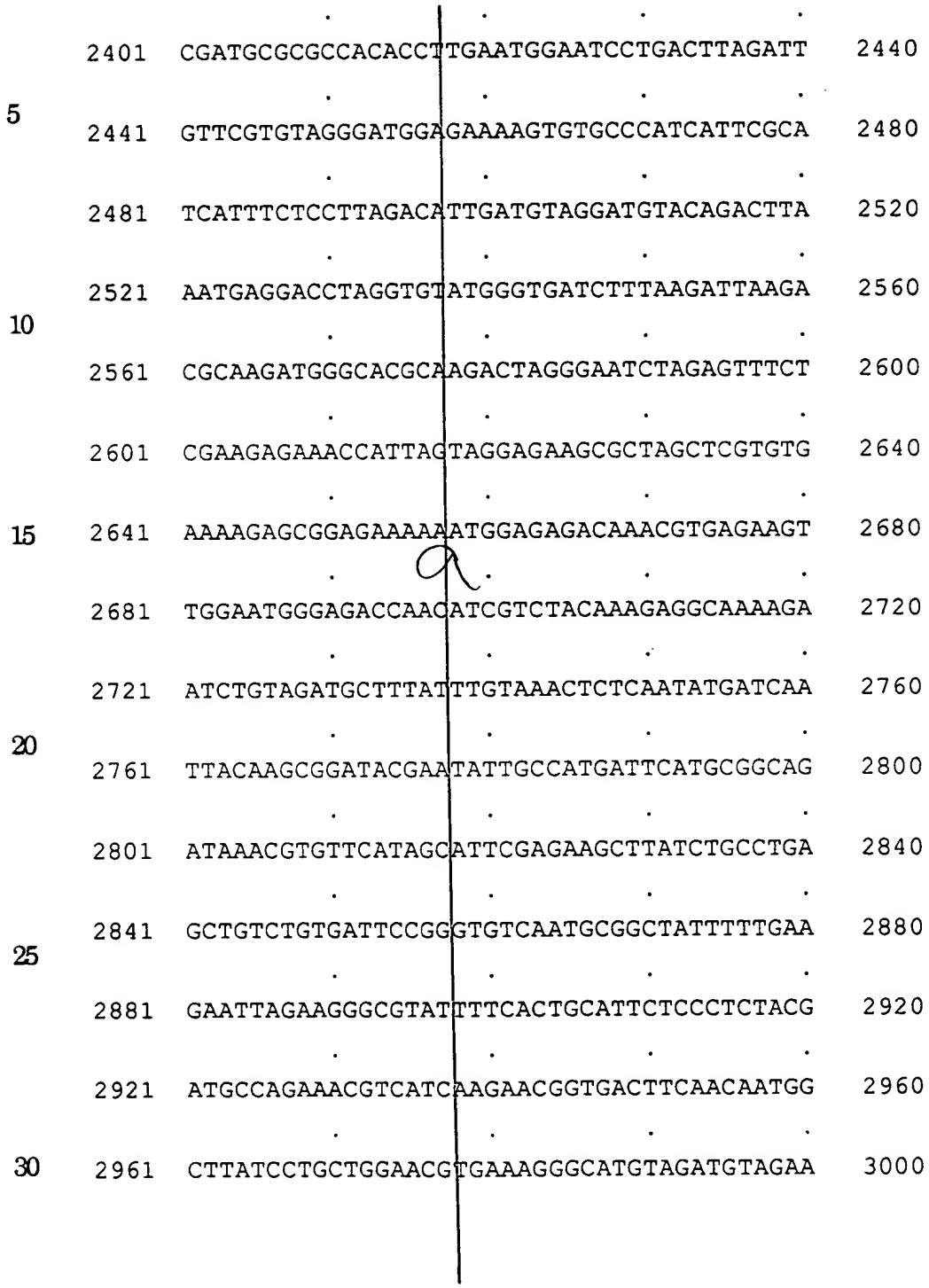
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2441 GTTCGTGTAGGGATGGAGAAAAGTGTGCCCATCATTCGCA 2480
2481 TCATTTCTCCTTAGACATTGATGTAGGATGTACAGACTTA 2520
2521 AATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGA 2560
2561 CGCAAGATGGGCACGCAAGACTAGGGAATCTAGAGTTTCT 2600
2601 CGAAGAGAAACCATTAGTAGGAGAAGCGCTAGCTCGTGTG 2640
2641 AAAAGAGCGGAGAAAAAATGGAGAGACAAACGTGAGAAGT 2680
2681 TGGAATGGGAGACCAACATCGTCTACAAAGAGGCAAAAGA 2720
2721 ATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAA 2760
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2801 ATAAACGTGTTCATAGCATTCGAGAAGCTTATCTGCCTGA 2840
2841 GCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTTGAA 2880
2881 GAATTAGAAGGGCGTATTTTCACTGCATTCTCCCTCTACG 2920
2921 ATGCCAGAAACGTCATCAAGAACGGTGACTTCAACAATGG 2960
2961 CTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAA 3000

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3001  GAACAAAACAACCAACGTTCGGTCCTTGTTGTTCCGGAAT  3040
3041  GGGAAGCAGAAGTGTCACAAGAAGTTCGTGTCTGTCCGGG  3080
3081  TCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGA  3120
3121  TATGGAGAAGGTTGCGTAACCATTCATGAGATCGAGAACA  3160
3161  ATACAGACGAACTGAAGTTTAGCAACTGCGTAGAAGAGGA  3200
3201  AATCTATCCAAATAACACGGTAACGTGTAATGATTATACT  3240
3241  GTAAATCAAGAAGAATACGGAGGTGCGTACACTTCTCGTA  3280
3281  ATCGAGGATATAACGAAGCTCCTTCCGTACCAGCTGATTA  3320
3321  TGCGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGA  3360
3361  AGAGAGAATCCTTGTGAATTTAACAGAGGGTATAGGGATT  3400
3401  ACACGCCACTACCAGTTGGTTATGTGACAAAAGAATTAGA  3440
3441  ATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGA  3480
3481  GAAACGGAAGGAACATTTATCGTGGACAGCGTGGAATTAC  3520
3521  TCCTTATGGAGGAA  3534.
```

20. A structural gene of Claim 13 encoding a full-length insecticidal protein of *B.t.*k. HD-73 having the sequence:

```
                .         .         .         .
      1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA   40
                .         .         .         .
     41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA   80
                .         .         .         .
     81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG   120
                .         .         .         .
    121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG   160
                .         .         .         .
    161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT   200
                .         .         .         .
    201 CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT   240
                .         .         .         .
    241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA   280
                .         .         .         .
    281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA   320
                .         .         .         .
    321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT   360
                .         .         .         .
    361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT   400
                .         .         .         .
    401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT   440
                .         .         .         .
    441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG   480
                .         .         .         .
    481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG   520
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521  ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCTGC  560
561  AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT  600
601  GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG  640
641  GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT  680
681  TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT  720
721  TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA  760
761  CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT  800
801  CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC  840
841  CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC  880
881  CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC  920
921  CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG  960
961  ATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTTTA  1000
1001 CCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCACA  1040
1041 ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA  1080
1081 ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG  1120
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1121  GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA  1160
1161  GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT  1200
1201  TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC  1240
1241  CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC  1280
1281  CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC  1320
1321  AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT  1360
1361  CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC  1400
1401  ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC  1440
1441  TTTCTCTTCAACGGTTCTGTCATTTCAGGACCAGGATTCA  1480
1481  CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA  1520
1521  CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTC  1560
1561  CCATCCACATCTACCAGATATAGAGTTCGTGTGAGGTATG  1600
1601  CTTCTGTGACCCCTATTCACCTCAACGTTAATTGGGGTAA  1640
1641  TTCATCCATCTTCTCCAATACAGTTCCAGCTACAGCTACC  1680
1681  TCCTTGGATAATCTCCAATCCAGCGATTTCGGTTACTTTG  1720
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1721  AAAGTGCCAATGCTTTTACATCTTCACTCGGTAACATCGT  1760
1761  GGGTGTTAGAAACTTTAGTGGGACTGCAGGAGTGATTATC  1800
1801  GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG  1840
1841  CTGAATATAATCTGGAAAGAGCGCAGAAGGCGGTGAATGC  1880
1881  GCTGTTTACGTCTACAAACCAACTAGGGCTAAAAACAAAT  1920
1921  GTAACGGATTATCATATTGATCAAGTGTCCAATTTAGTTA  1960
1961  CGTATTTATCGGATGAATTTTGTCTGGATGAAAAGCGAGA  2000
2001  ATTGTCCGAGAAAGTCAAACATGCGAAGCGACTCAGTGAT  2040
2041  GAACGCAATTTACTCCAAGATTCAAATTTCAAAGACATTA  2080
2081  ATAGGCAACCAGAACGTGGGTGGGGCGGAAGTACAGGGAT  2120
2121  TACCATCCAAGGAGGGGATGACGTATTTAAAGAAAATTAC  2160
2161  GTCACACTATCAGGTACCTTTGATGAGTGCTATCCAACAT  2200
2201  ATTTGTATCAAAAAATCGATGAATCAAAATTAAAAGCCTT  2240
2241  TACCCGTTATCAATTAAGAGGGTATATCGAAGATAGTCAA  2280
2281  GACTTAGAAATCTATTTAATTCGCTACAATGCAAAACATG  2320
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2441  GTTCGTGTAGGGATGGAGAAAAGTGTGCCCATCATTCGCA  2480
2481  TCATTTCTCCTTAGACATTGATGTAGGATGTACAGACTTA  2520
2521  AATGAGGACCTAGGTGTATGGGTGATCTTTAAGATTAAGA  2560
2561  CGCAAGATGGGCACGCAAGACTAGGGAATCTAGAGTTTCT  2600
2601  CGAAGAGAAACCATTAGTAGGAGAAGCGCTAGCTCGTGTG  2640
2641  AAAAGAGCGGAGAAAAAATGGAGAGACAAACGTGAAAAAT  2680
2681  TGGAATGGGAAACAAATATCGTTTATAAAGAGGCAAAAGA  2720
2721  ATCTGTAGATGCTTTATTTGTAAACTCTCAATATGATCAA  2760
2761  TTACAAGCGGATACGAATATTGCCATGATTCATGCGGCAG  2800
2801  ATAAACGTGTTCATAGCATTCGAGAAGCTTATCTGCCTGA  2840
2841  GCTGTCTGTGATTCCGGGTGTCAATGCGGCTATTTTTGAA  2880
2881  GAATTAGAAGGGCGTATTTTCACTGCATTCTCCCTATATG  2920
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2921  ATGCGAGAAATGTCATTAAAAATGGTGATTTTAATAATGG  2960
2961  CTTATCCTGCTGGAACGTGAAAGGGCATGTAGATGTAGAA  3000
3001  GAACAAAACAACCAACGTTCGGTCCTTGTTGTTCCGGAAT  3040
3041  GGGAAGCAGAAGTGTCACAAGAAGTTCGTGTCTGTCCGGG  3080
3081  TCGTGGCTATATCCTTCGTGTCACAGCGTACAAGGAGGGA  3120
3121  TATGGAGAAGGTTGCGTAACCATTCATGAGATCGAGAACA  3160
3161  ATACAGACGAACTGAAGTTTAGCAACTGCGTAGAAGAGGA  3200
3201  AATCTATCCAAATAACACGGTAACGTGTAATGATTATACT  3240
3241  GTAAATCAAGAAGAATACGGAGGTGCGTACACTTCTCGTA  3280
3281  ATCGAGGATATAACGAAGCTCCTTCCGTACCAGCTGATTA  3320
3321  TGCGTCAGTCTATGAAGAAAAATCGTATACAGATGGACGA  3360
3361  AGAGAGAATCCTTGTGAATTTAACAGAGGGTATAGGGATT  3400
3401  ACACGCCACTACCAGTTGGTTATGTGACAAAAGAATTAGA  3440
3441  ATACTTCCCAGAAACCGATAAGGTATGGATTGAGATTGGA  3480
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3481 GAAACGGAAGGAACATTTATCGTGGACAGCGTGGAATTAC 3520

3521 TCCTTATGGAGGAA 3534.

21. A structural gene of Claim 13 encoding a full-length insecticidal protein of *B.t.k.* HD-73 having the sequence:

1 ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA 40

41 ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA 80

81 ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG 120

121 TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG 160

161 CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT 200

201 CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT 240

241 GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA 280

281 ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA 320

321 CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT 360

361 CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT 400

401 TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT 440

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441  GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG  480
481  TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG  520
521  ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCTGC  560
561  AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT  600
601  GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG  640
641  GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT  680
681  TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT  720
721  TTGGACATTGTGTCTCTCTTCCCGAACTATGACTCCAGAA  760
761  CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT  800
801  CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC  840
841  CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC  880
881  CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC  920
921  CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG  960
961  ATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTTTA  1000
1001 CCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCACA  1040
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1041  ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA  1080
1081  ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG  1120
1121  GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA  1160
1161  GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT  1200
1201  TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC  1240
1241  CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC  1280
1281  CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC  1320
1321  AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT  1360
1361  CTTGGATACACCGTAGTGCTGAGTTCAACAACATCATCGC  1400
1401  ATCCGATAGTATTACTCAAATCCCTGCAGTGAAGGGAAAC  1440
1441  TTTCTCTTCAACGGTTCTGTCATTTCAGGACCAGGATTCA  1480
1481  CTGGTGGAGACCTCGTTAGACTCAACAGCAGTGGAAATAA  1520
1521  CATTCAGAATAGAGGGTATATTGAAGTTCCAATTCACTTC  1560
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1601  CTTCTGTGACCCCTATTCACCTCAACGTTAATTGGGGTAA  1640
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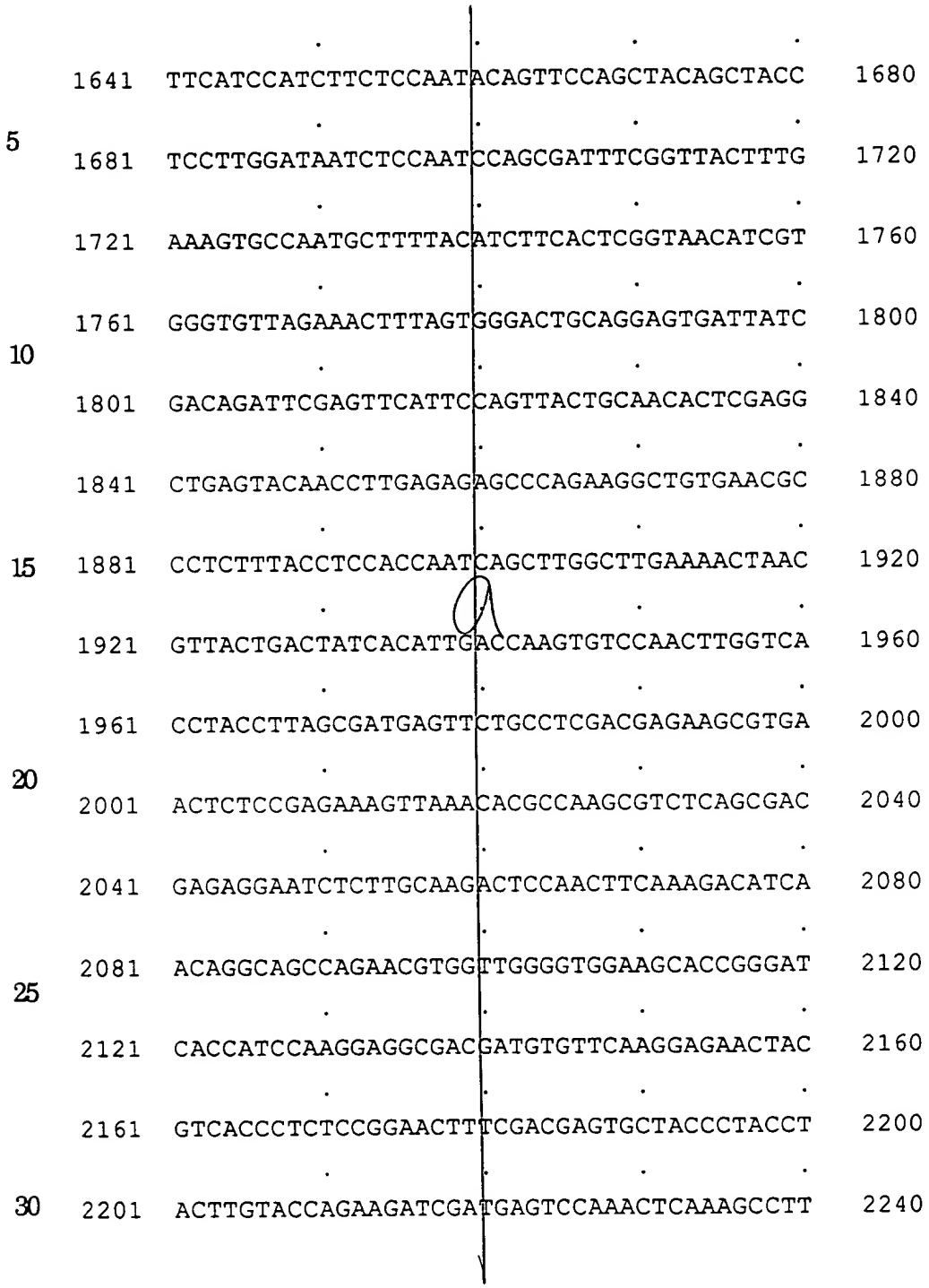
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1761 GGGTGTTAGAAACTTTAGTGGGACTGCAGGAGTGATTATC 1800
1801 GACAGATTCGAGTTCATTCCAGTTACTGCAACACTCGAGG 1840
1841 CTGAGTACAACCTTGAGAGAGCCCAGAAGGCTGTGAACGC 1880
1881 CCTCTTTACCTCCACCAATCAGCTTGGCTTGAAAACTAAC 1920
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1961 CCTACCTTAGCGATGAGTTCTGCCTCGACGAGAAGCGTGA 2000
2001 ACTCTCCGAGAAAGTTAAACACGCCAAGCGTCTCAGCGAC 2040
2041 GAGAGGAATCTCTTGCAAGACTCCAACTTCAAAGACATCA 2080
2081 ACAGGCAGCCAGAACGTGGTTGGGGTGGAAGCACCGGGAT 2120
2121 CACCATCCAAGGAGGCGACGATGTGTTCAAGGAGAACTAC 2160
2161 GTCACCCTCTCCGGAACTTTCGACGAGTGCTACCCTACCT 2200
2201 ACTTGTACCAGAAGATCGATGAGTCCAAACTCAAAGCCTT 2240

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2241  CACCAGGTATCAACTTAGAGGCTACATCGAAGACAGCCAA  2280
2281  GACCTTGAAATCTACTCGATCAGGTACAATGCCAAGCACG  2320
2321  AGACCGTGAATGTCCCAGGTACTGGTTCCCTCTGGCCACT  2360
2361  TTCTGCCCAATCTCCCATTGGGAAGTGTGGAGAGCCTAAC  2400
2401  AGATGCGCTCCACACCTTGAGTGGAATCCTGACTTGGACT  2440
2441  GCTCCTGCAGGGATGGCGAGAAGTGTGCCCACCATTCTCA  2480
2481  TCACTTCTCCTTGGACATCGATGTGGGATGTACTGACCTG  2520
2521  AATGAGGACCTCGGAGTCTGGGTCATCTTCAAGATCAAGA  2560
2561  CCCAAGACGGACACGCAAGACTTGGCAACCTTGAGTTTCT  2600
2601  CGAAGAGAAACCATTGGTCGGTGAAGCTCTCGCTCGTGTG  2640
2641  AAGAGAGCAGAGAAGAAGTGGAGGGACAAACGTGAGAAAC  2680
2681  TCGAATGGGAAACTAACATCGTTTACAAGGAGGCCAAAGA  2720
2721  GTCCGTGGATGCTTTGTTCGTGAACTCCCAATATGATCAG  2760
2761  TTGCAAGCCGACACCAACATCGCCATGATCCACGCCGCAG  2800
2801  ACAAACGTGTGCACAGCATTCGTGAGGCTTACTTGCCTGA  2840
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2841  GTTGTCCGTGATCCCTGGTGTGAACGCTGCCATCTTCGAG  2880
2881  GAACTTGAGGGACGTATCTTTACCGCATTCTCCTTGTACG  2920
2921  ATGCCAGAAACGTCATCAAGAACGGTGACTTCAACAATGG  2960
2961  CCTCAGCTGCTGGAATGTGAAAGGTCATGTGGACGTGGAG  3000
3001  GAACAGAACAATCAGCGTTCCGTCCTGGTTGTGCCTGAGT  3040
3041  GGGAAGCTGAAGTGTCCCAAGAGGTTAGAGTCTGTCCAGG  3080
3081  TAGAGGCTACATTCTCCGTGTGACCGCTTACAAGGAGGGA  3120
3121  TACGGTGAGGGTTGCGTGACCATCCACGAGATCGAGAACA  3160
3161  ACACCGACGAGCTTAAGTTCTCCAACTGCGTCGAGGAAGA  3200
3201  AATCTATCCCAACAACACCGTTACTTGCAACGACTACACT  3240
3241  GTGAATCAGGAAGAGTACGGAGGTGCCTACACTAGCCGTA  3280
3281  ACAGAGGTTACAACGAAGCTCCTTCCGTTCCTGCTGACTA  3320
3321  TGCCTCCGTGTACGAGGAGAAATCCTACACAGATGGCAGA  3360
3361  CGTGAGAACCCTTGCGAGTTCAACAGAGGTTACAGGGACT  3400
3401  ACACACCACTTCCAGTTGGCTATGTTACCAAGGAGCTTGA  3440
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3441 GTACTTTCCTGAGACCGACAAAGTGTGGATCGAGATCGGT 3480

3481 GAAACCGAGGGAACCTTCATCGTGGACAGCGTGGAGCTTC 3520

3521 TCTTGATGGAGGAA 3534.

22. A structural gene of Claim 13 which encodes an insecticidal protein of *B.t.t.* having the sequence:

1 ATGACTGCAGACAACAACACCGAAGCCCTCGACAGTTCTA 40

41 CCACTAAGGATGTTATCCAGAAGGGTATCTCCGTTGTGGG 80

81 AGACCTCTTGGGCGTGGTTGGATTTCCCTTCGGTGGAGCC 120

121 CTCGTGAGCTTCTATACAAACTTTCTCAACACCATTTGGC 160

161 CAAGCGAGGACCCTTGGAAAGCATTCATGGAGCAAGTTGA 200

201 AGCTCTTATGGATCAGAAGATTGCAGATTATGCCAAGAAC 240

241 AAGGCTTTGGCAGAACTCCAGGGCCTTCAGAACAATGTGG 280

281 AGGACTACGTGAGTGCATTGTCCAGCTGGCAGAAGAACCC 320

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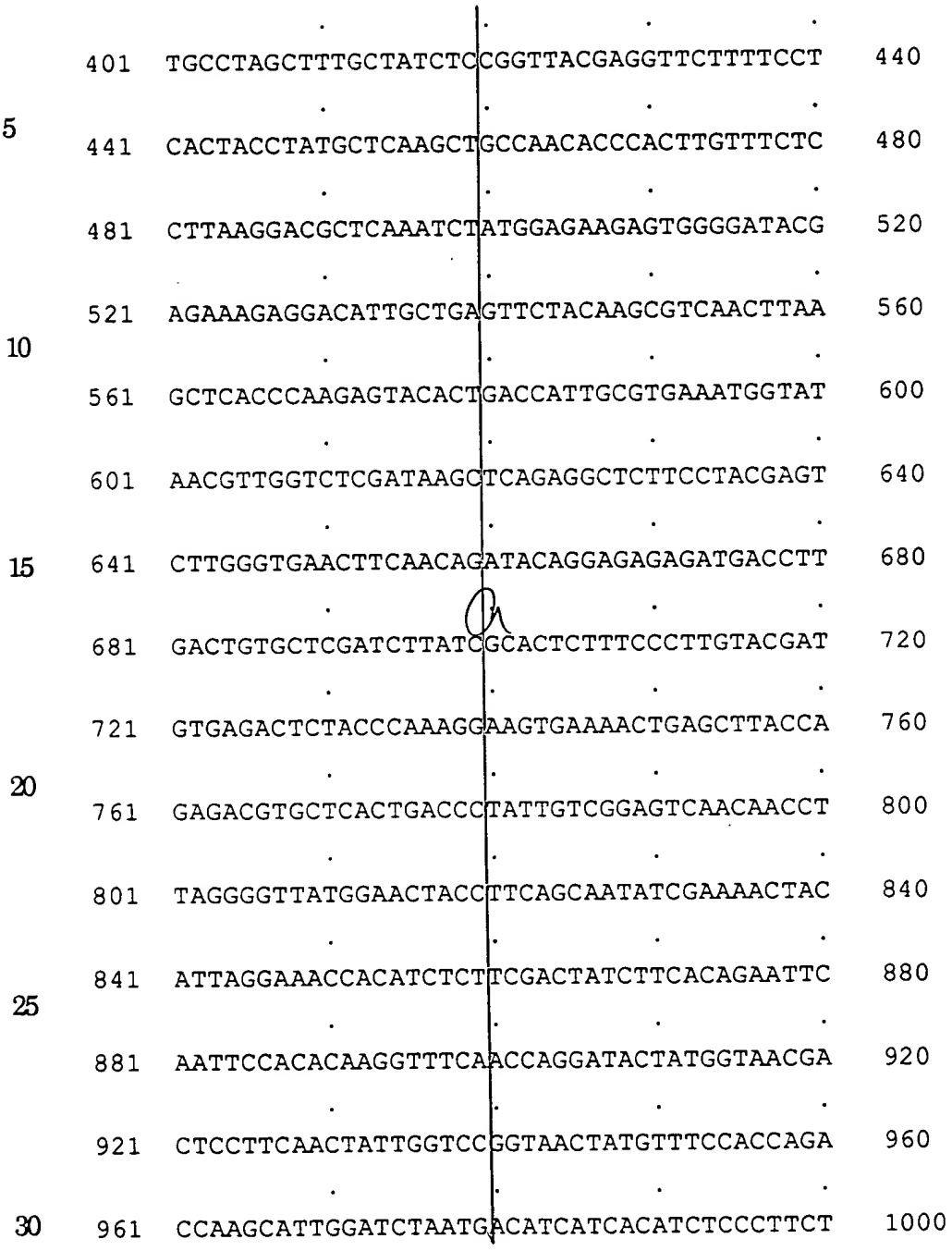
361 GAGTTGTTCTCTCAAGCCGAATCCCACTTCAGAAATTCCA 400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521 AGAAAGAGGACATTGCTGAGTTCTACAAGCGTCAACTTAA 560
561 GCTCACCCAAGAGTACACTGACCATTGCGTGAAATGGTAT 600
601 AACGTTGGTCTCGATAAGCTCAGAGGCTCTTCCTACGAGT 640
641 CTTGGGTGAACTTCAACAGATACAGGAGAGAGATGACCTT 680
681 GACTGTGCTCGATCTTATCGCACTCTTTCCCTTGTACGAT 720
721 GTGAGACTCTACCCAAAGGAAGTGAAAACTGAGCTTACCA 760
761 GAGACGTGCTCACTGACCCTATTGTCGGAGTCAACAACCT 800
801 TAGGGGTTATGGAACTACCTTCAGCAATATCGAAAACTAC 840
841 ATTAGGAAACCACATCTCTTCGACTATCTTCACAGAATTC 880
881 AATTCCACACAAGGTTTCAACCAGGATACTATGGTAACGA 920
921 CTCCTTCAACTATTGGTCCGGTAACTATGTTTCCACCAGA 960
961 CCAAGCATTGGATCTAATGACATCATCACATCTCCCTTCT 1000

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1001  ATGGTAACAAGTCCAGTGAACCTGTGCAGAACCTTGAGTT  1040
1041  CAACGGCGAGAAAGTCTATAGAGCCGTCGCAAACACCAAT  1080
1081  CTCGCTGTGTGGCCATCCGCAGTTTACTCAGGCGTCACAA  1120
1121  AGGTGGAGTTTAGTCAGTATAACGATCAGACCGATGAGGC  1160
1161  CAGCACCCAGACTTACGACTCCAAACGTAACGTTGGCGCA  1200
1201  GTCTCTTGGGATTCTATCGACCAATTGCCTCCAGAAACCA  1240
1241  CAGACGAACCATTGGAGAAGGGCTACAGCCACCAACTTAA  1280
1281  CTATGTGATGTGCTTCTTGATGCAAGGTTCCAGAGGGACC  1320
1321  ATTCCAGTGTTGACCTGGACACACAAGTCCGTGGACTTCT  1360
1361  TCAACATGATCGATAGCAAGAAGATCACTCAACTTCCCTT  1400
1401  GGTGAAAGCCTACAAGCTGCAATCTGGTGCTTCCGTTGTC  1440
1441  GCAGGTCCCAGATTCACTGGAGGTGACATCATCCAGTGCA  1480
1481  CAGAGAACGGCAGCGCAGCTACTATCTACGTGACACCTGA  1520
1521  TGTGTCTTACTCTCAGAAGTACAGGGCACGTATTCATTAC  1560
1561  GCATCTACCAGCCAGATCACCTTCACACTCAGCTTGGATG  1600
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1601  GAGCACCCTTCAACCAGTATTACTTTGACAAGACCATCAA  1640
1641  CAAAGGTGACACTCTCACATACAATAGCTTCAACTTGGCA  1680
1681  AGTTTCAGCACACCATTTGAACTCTCAGGCAACAATCTTC  1720
1721  AGATCGGCGTCACCGGTCTCAGCGCCGGAGACAAAGTCTA  1760
1761  CATCGACAAGATTGAGTTCATCCCAGTGAAC  1791.
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23. A structural gene of Claim 13 which encodes an insecticidal protein of *B.t.* entomocidus having the sequence:

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   1  ATGGAGGAGAACAACCAAAACCAATGCATTCCATACAACT   40
  41  GCTTGAGTAACCCAGAAGAGGTATTGCTTGATGGAGAACG   80
  81  CATTTCAACCGGTAACTCTTCCATCGACATCTCCTTGTCC  120
 121  TTGGTCCAGTTTCTGGTCAGCAACTTCGTGCCAGGTGGTG  160
 161  GGTTCCTTGTCGGACTAATTGACTTCGTCTGGGGTATCGT  200
 201  TGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATTGAG  240
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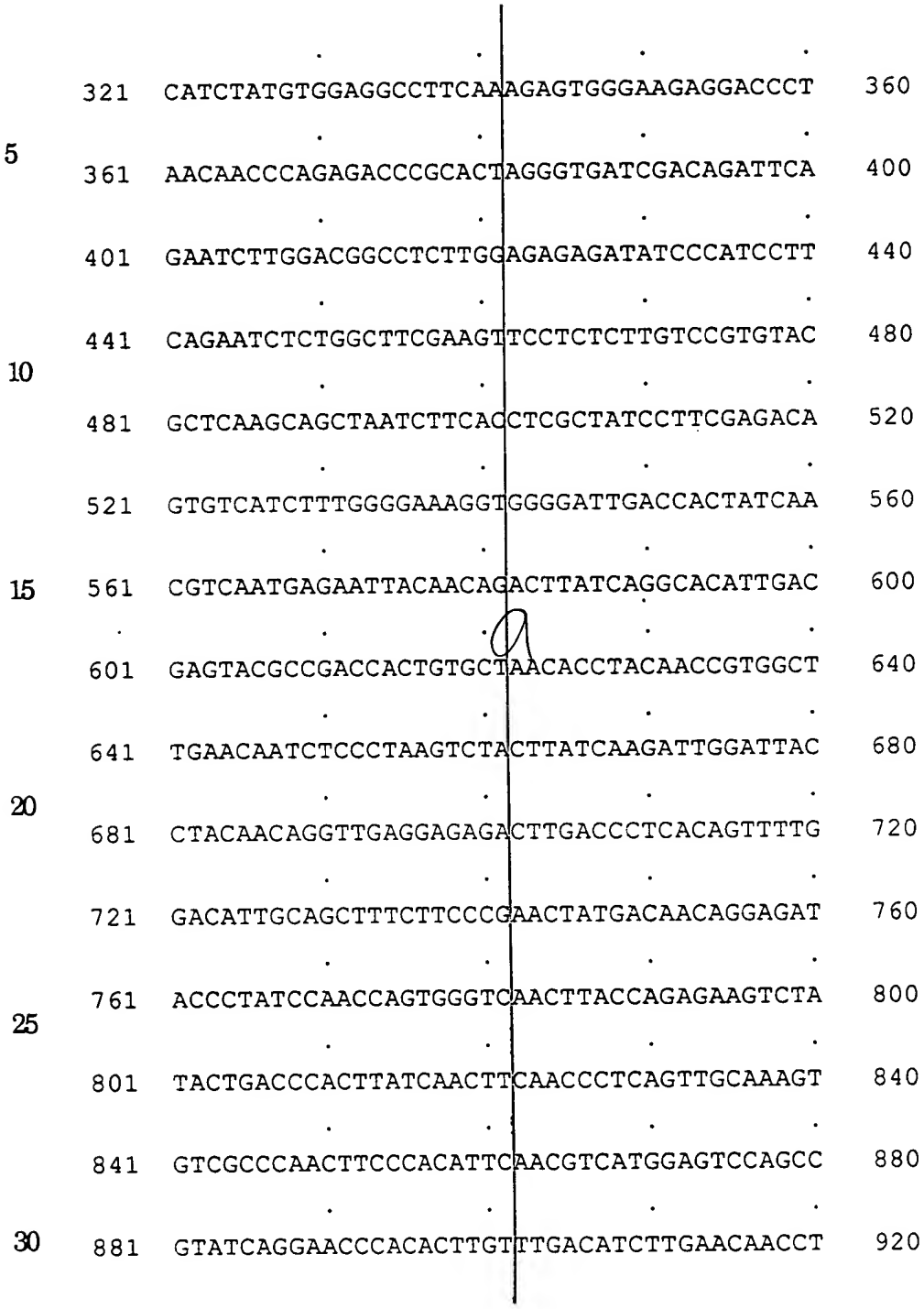
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441 CAGAATCTCTGGCTTCGAAGTTCCTCTCTTGTCCGTGTAC 480
481 GCTCAAGCAGCTAATCTTCACCTCGCTATCCTTCGAGACA 520
521 GTGTCATCTTTGGGGAAAGGTGGGGATTGACCACTATCAA 560
561 CGTCAATGAGAATTACAACAGACTTATCAGGCACATTGAC 600
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641 TGAACAATCTCCCTAAGTCTACTTATCAAGATTGGATTAC 680
681 CTACAACAGGTTGAGGAGAGACTTGACCCTCACAGTTTTG 720
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801 TACTGACCCACTTATCAACTTCAACCCTCAGTTGCAAAGT 840
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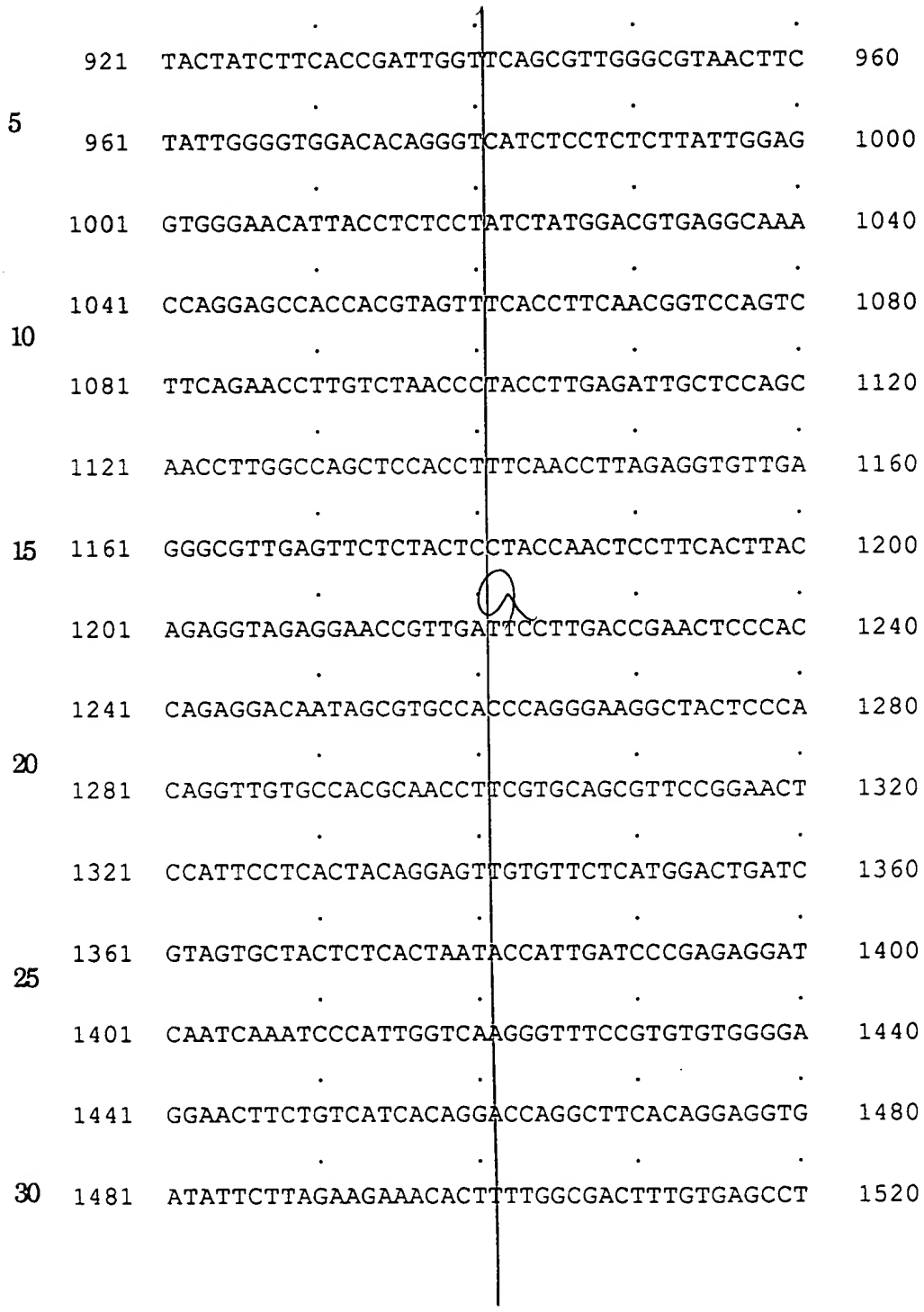
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1041 CCAGGAGCCACCACGTAGTTTCACCTTCAACGGTCCAGTC 1080
1081 TTCAGAACCTTGTCTAACCCTACCTTGAGATTGCTCCAGC 1120
1121 AACCTTGGCCAGCTCCACCTTTCAACCTTAGAGGTGTTGA 1160
1161 GGGCGTTGAGTTCTCTACTCCTACCAACTCCTTCACTTAC 1200
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1241 CAGAGGACAATAGCGTGCCACCCAGGGAAGGCTACTCCCA 1280
1281 CAGGTTGTGCCACGCAACCTTCGTGCAGCGTTCCGGAACT 1320
1321 CCATTCCTCACTACAGGAGTTGTGTTCTCATGGACTGATC 1360
1361 GTAGTGCTACTCTCACTAATACCATTGATCCCGAGAGGAT 1400
1401 CAATCAAATCCCATTGGTCAAGGGTTTCCGTGTGTGGGGA 1440
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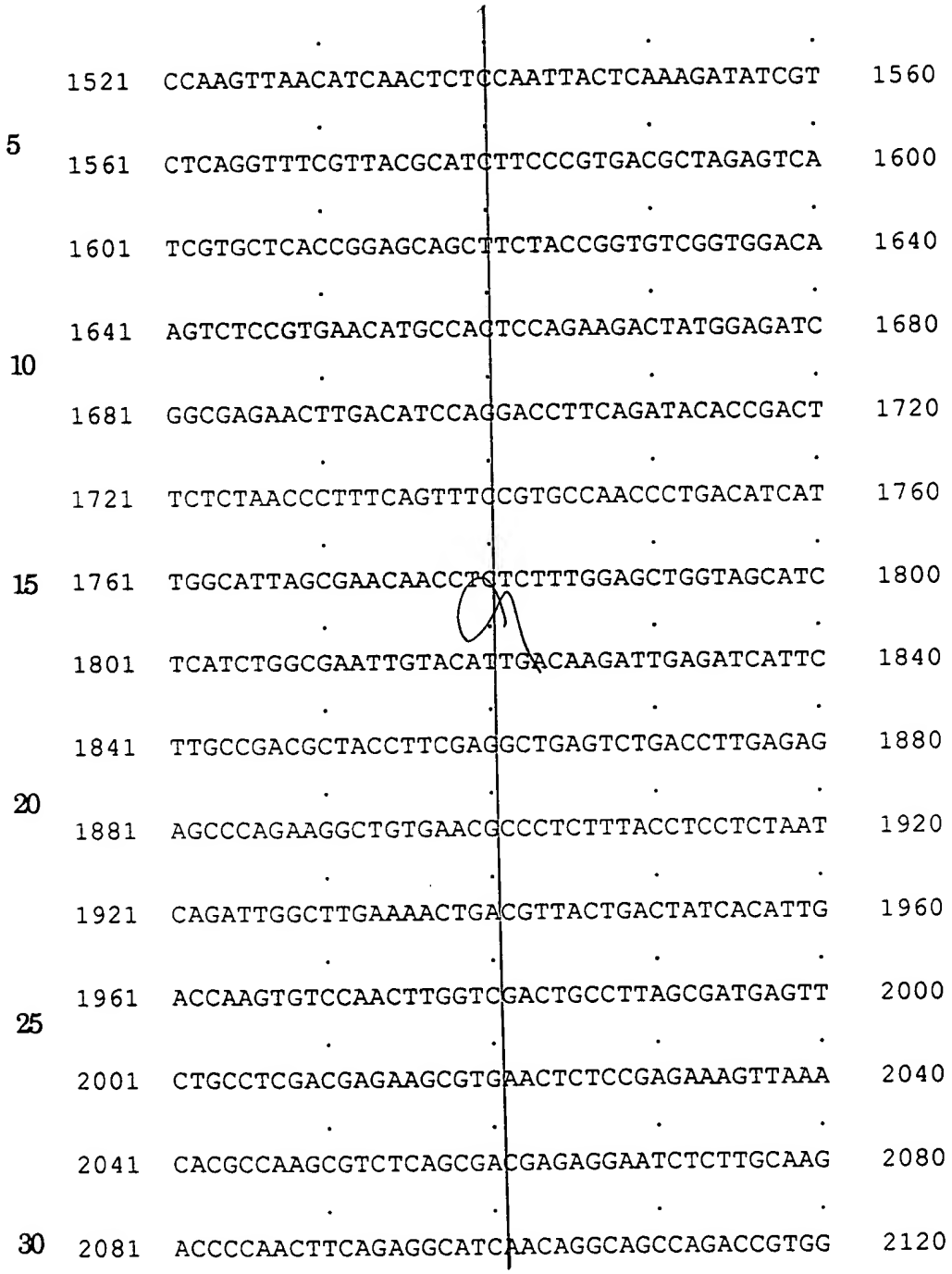
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1641 AGTCTCCGTGAACATGCCACTCCAGAAGACTATGGAGATC 1680
1681 GGCGAGAACTTGACATCCAGGACCTTCAGATACACCGACT 1720
1721 TCTCTAACCCTTTCAGTTTCCGTGCCAACCCTGACATCAT 1760
1761 TGGCATTAGCGAACAACCTCTCTTTGGAGCTGGTAGCATC 1800
1801 TCATCTGGCGAATTGTACATTGACAAGATTGAGATCATTC 1840
1841 TTGCCGACGCTACCTTCGAGGCTGAGTCTGACCTTGAGAG 1880
1881 AGCCCAGAAGGCTGTGAACGCCCTCTTTACCTCCTCTAAT 1920
1921 CAGATTGGCTTGAAAACTGACGTTACTGACTATCACATTG 1960
1961 ACCAAGTGTCCAACTTGGTCGACTGCCTTAGCGATGAGTT 2000
2001 CTGCCTCGACGAGAAGCGTGAACTCTCCGAGAAAGTTAAA 2040
2041 CACGCCAAGCGTCTCAGCGACGAGAGGAATCTCTTGCAAG 2080
2081 ACCCCAACTTCAGAGGCATCAACAGGCAGCCAGACCGTGG 2120

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2121  TTGGAGAGGAAGCACCGACATCACCATCCAAGGAGGCGAC  2160
2161  GATGTGTTCAAGGAGAACTACGTCACCCTCCCAGGAACTG  2200
2201  TGGACGAGTGCTACCCTACCTACTTGTACCAGAAGATCGA  2240
2241  TGAGTCCAAACTCAAAGCCTACACCAGGTATGAACTTAGA  2280
2281  GGCTACATCGAAGACAGCCAAGACCTTGAAATCTACCTCA  2320
2321  TCAGGTACAATGCCAAGCACGAGATCGTGAATGTCCCAGG  2360
2361  TACTGGTTCCCTCTGGCCACTTTCTGCCCAAATGCCCATT  2400
2401  GGGAAGTGTGGAGAGCCTAACAGATGCGCTCCACACCTTG  2440
2441  AGTGGAATCCTGACTTGGACTGCTCCTGCAGGGATGGCGA  2480
2481  GAAGTGTGCCCACCATTCTCATCACTTCACCTTGGACATC  2520
2521  GATGTGGGATGTACTGACCTGAATGAGGACCTCGGAGTCT  2560
2561  GGGTCATCTTCAAGATCAAGACCCAAGACGGACACGCAAG  2600
2601  ACTTGGCAACCTTGAGTTTCTCGAAGAGAAACCATTGCTC  2640
2641  GGTGAAGCTCTCGCTCGTGTGAAGAGAGCAGAGAAGAAGT  2680
2681  GGAGGGACAAACGTGAGAAACTCCAACTCGAGACTAACAT  2720
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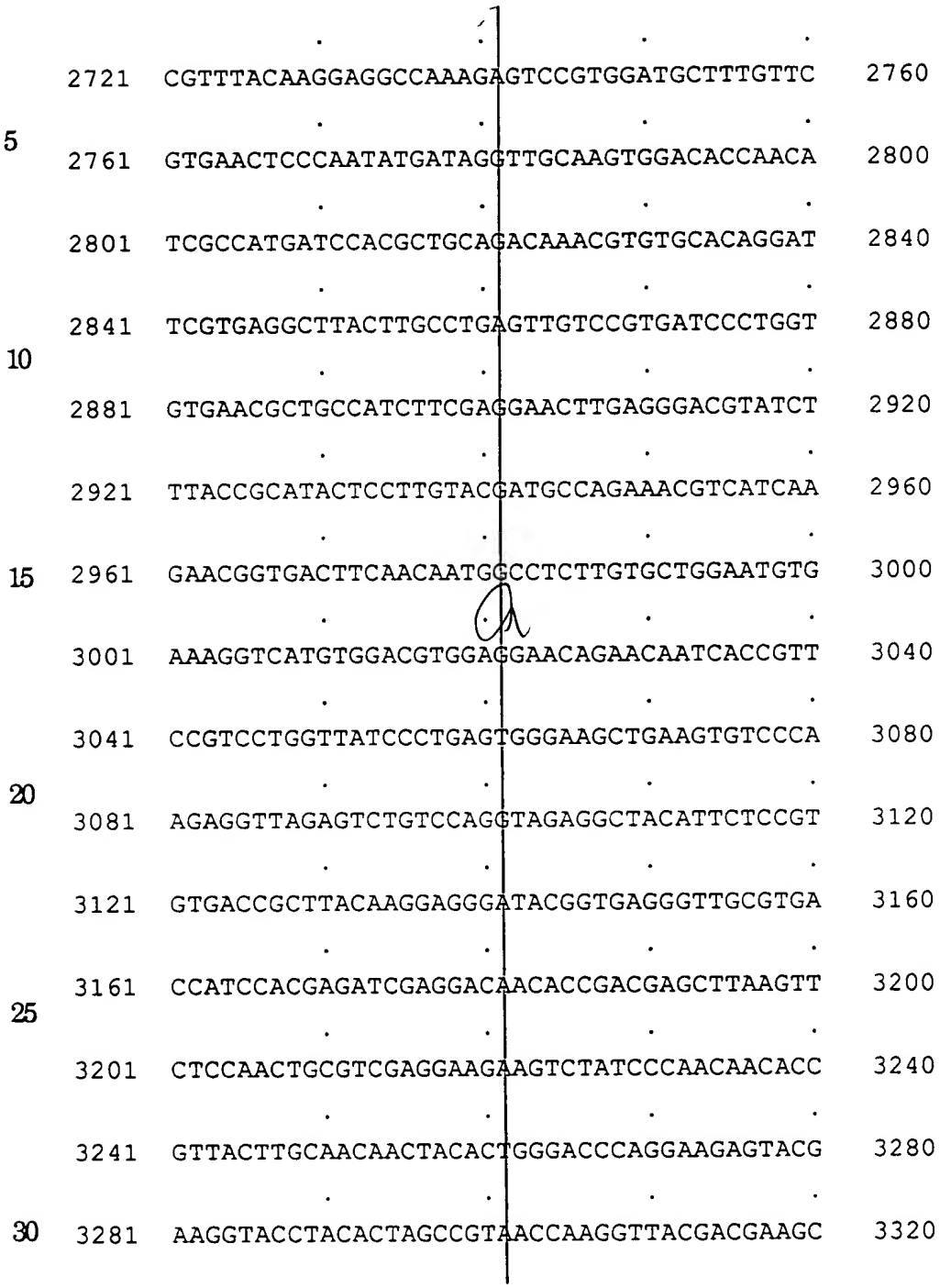
2721 CGTTTACAAGGAGGCCAAAGAGTCCGTGGATGCTTTGTTC 2760
2761 GTGAACTCCCAATATGATAGGTTGCAAGTGGACACCAACA 2800
2801 TCGCCATGATCCACGCTGCAGACAAACGTGTGCACAGGAT 2840
2841 TCGTGAGGCTTACTTGCCTGAGTTGTCCGTGATCCCTGGT 2880
2881 GTGAACGCTGCCATCTTCGAGGAACTTGAGGGACGTATCT 2920
2921 TTACCGCATACTCCTTGTACGATGCCAGAAACGTCATCAA 2960
2961 GAACGGTGACTTCAACAATGGCCTCTTGTGCTGGAATGTG 3000
3001 AAAGGTCATGTGGACGTGGAGGAACAGAACAATCACCGTT 3040
3041 CCGTCCTGGTTATCCCTGAGTGGGAAGCTGAAGTGTCCCA 3080
3081 AGAGGTTAGAGTCTGTCCAGGTAGAGGCTACATTCTCCGT 3120
3121 GTGACCGCTTACAAGGAGGGATACGGTGAGGGTTGCGTGA 3160
3161 CCATCCACGAGATCGAGGACAACACCGACGAGCTTAAGTT 3200
3201 CTCCAACTGCGTCGAGGAAGAAGTCTATCCCAACAACACC 3240
3241 GTTACTTGCAACAACTACACTGGGACCCAGGAAGAGTACG 3280
3281 AAGGTACCTACACTAGCCGTAACCAAGGTTACGACGAAGC 3320

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3321  TTACGGAAACAATCCTTCCGTTCCTGCTGACTATGCCTCC  3360
3361  GTGTACGAGGAGAAATCCTACACAGATGGCAGACGTGAGA  3400
3401  ACCCTTGCGAGTCCAACAGAGGTTACGGTGACTACACACC  3440
3441  ACTTCCAGCAGGCTATGTTACCAAGGACCTTGAGTACTTT  3480
3481  CCTGAGACCGACAAAGTGTGGATCGAGATCGGTGAAACCG  3520
3521  AGGGAACCTTCATCGTGGACAGCGTGGAGCTTCTCTTGAT  3560
3561  GGAGGAA  3567.
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24. A structural gene of Claim 13 which encodes a P2 insecticidal protein having the sequence:

```
   1  ATGGACAACAACGTCTTGAACTCTGGTAGAACAACCATCT   40
  41  GCGACGCATACAACGTCGTGGCTCACGATCCATTCAGCTT   80
  81  CGAACACAAGAGCCTCGACACTATTCAGAAGGAGTGGATG  120
 121  GAATGGAAACGTACTGACCACTCTCTCTACGTCGCACCTG  160
 161  TGGTTGGAACAGTGTCCAGCTTCCTTCTCAAGAAGGTCGG  200
 201  CTCTCTCATCGGAAAACGTATCTTGTCCGAACTCTGGGGT  240
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241  ATCATCTTTCCATCTGGGTCCACTAATCTCATGCAAGACA  280
281  TCTTGAGGGAGACCGAACAGTTTCTCAACCAGCGTCTCAA  320
321  CACTGATACCTTGGCTAGAGTCAACGCTGAGTTGATCGGT  360
361  CTCCAAGCAAACATTCGTGAGTTCAACCAGCAAGTGGACA  400
401  ACTTCTTGAATCCAACTCAGAATCCTGTGCCTCTTTCCAT  440
441  CACTTCTTCCGTGAACACTATGCAGCAACTCTTCCTCAAC  480
                    G
481  AGATTGCCTCAGTTTCAGATTCAAGGCTACCAGTTGCTCC  520
521  TTCTTCCACTCTTTGCTCAGGCTGCCAACATGCACTTGTC  560
561  CTTCATACGTGACGTGATGCTCAACGCTGACGAATGGGGA  600
601  ATCTCTGCAGCCACTCTTAGGACATACAGAGACTACTTGA  640
641  GGAACTACACTCGTGATTACTCCAACTATTGCATCAACAC  680
681  TTATCAGACTGCCTTTCGTGGACTCAATACTAGGCTTCAC  720
721  GACATGCTTGAGTTCAGGACCTACATGTTCCTTAACGTGT  760
761  TTGAGTACGTCAGCATTTGGAGTCTCTTCAAGTACCAGAG  800
801  CTTGATGGTGTCCTCTGGAGCCAATCTCTACGCCTCTGGC  840
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841  AGTGGACCACAGCAAACTCAGAGCTTCACAGCTCAGAACT  880
881  GGCCATTCTTGTATAGCTTGTTCCAAGTCAACTCCAACTA  920
921  CATTCTCAGTGGTATCTCTGGGACCAGACTCTCCATAACC  960
961  TTTCCCAACATTGGTGGACTTCCAGGCTCCACTACAACCC  1000
1001 ATAGCCTTAACTCTGCCAGAGTGAACTACAGTGGAGGTGT  1040
1041 CAGCTCTGGATTGATTGGTGCAACTAACTTGAACCACAAC  1080
1081 TTCAATTGCTCCACCGTCTTGCCACCTCTGAGCACACCGT  1120
1121 TTGTGAGGTCCTGGCTTGACAGCGGTACTGATCGCGAAGG  1160
1161 AGTTGCTACCTCTACAAACTGGCAAACCGAGTCCTTCCAA  1200
1201 ACCACTCTTAGCCTTCGGTGTGGAGCTTTCTCTGCACGTG  1240
1241 GGAATTCAAACTACTTTCCAGACTACTTCATTAGGAACAT  1280
1281 CTCTGGTGTTCCTCTCGTCATCAGGAATGAAGACCTCACC  1320
1321 CGTCCACTTCATTACAACCAGATTAGGAACATCGAGTCTC  1360
1361 CATCCGGTACTCCAGGAGGTGCAAGAGCTTACCTCGTGTC  1400
1401 TGTCCATAACAGGAAGAACAACATCTACGCTGCCAACGAG  1440
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1441  AATGGCACCATGATTCACCTTGCACCAGAAGATTACACTG  1480
1481  GATTCACCATCTCTCCAATCCATGCTACCCAAGTGAACAA  1520
1521  TCAGACACGCACCTTCATCTCCGAAAAGTTCGGAAATCAA  1560
1561  GGTGACTCCTTGAGGTTCGAGCAATCCAACACTACCGCTA  1600
1601  GGTACACTTTGAGAGGCAATGGAAACAGCTACAACCTTTA  1640
1641  CTTGAGAGTTAGCTCCATTGGTAACTCCACCATCCGTGTT  1680
1681  ACCATCAACGGACGTGTTTACACAGTCTCTAATGTGAACA  1720
1721  CTACAACGAACAATGATGGCGTTAACGACAACGGAGCCAG  1760
1761  ATTCAGCGACATCAACATTGGCAACATCGTGGCCTCTGAC  1800
1801  AACACTAACGTTACTTTGGACATCAATGTGACCCTCAATT  1840
1841  CTGGAACTCCATTTGATCTCATGAACATCATGTTTGTGCC  1880
1881  AACTAACCTCCCTCCATTGTACTAA  1905.
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25. A plant transformation vector comprising a plant gene containing a structural gene of Claim 13.

26. A structural gene sequence of Claim 13 encoding a fusion protein comprising the N-terminal 610 amino acids of *B.t.k.* HD-1 and the C-terminal 567 amino acids of *B.t.k.* HD-73, said gene having the sequence:

```
   1  ATGGACAACAACCCAAACATCAACGAATGCATTCCATACA   40
  41  ACTGCTTGAGTAACCCAGAAGTTGAAGTACTTGGTGGAGA   80
  81  ACGCATTGAAACCGGTTACACTCCCATCGACATCTCCTTG  120
 121  TCCTTGACACAGTTTCTGCTCAGCGAGTTCGTGCCAGGTG  160
 161  CTGGGTTCGTTCTCGGACTAGTTGACATCATCTGGGGTAT  200
 201  CTTTGGTCCATCTCAATGGGATGCATTCCTGGTGCAAATT  240
 241  GAGCAGTTGATCAACCAGAGGATCGAAGAGTTCGCCAGGA  280
 281  ACCAGGCCATCTCTAGGTTGGAAGGATTGAGCAATCTCTA  320
 321  CCAAATCTATGCAGAGAGCTTCAGAGAGTGGGAAGCCGAT  360
 361  CCTACTAACCCAGCTCTCCGCGAGGAAATGCGTATTCAAT  400
 401  TCAACGACATGAACAGCGCCTTGACCACAGCTATCCCATT  440
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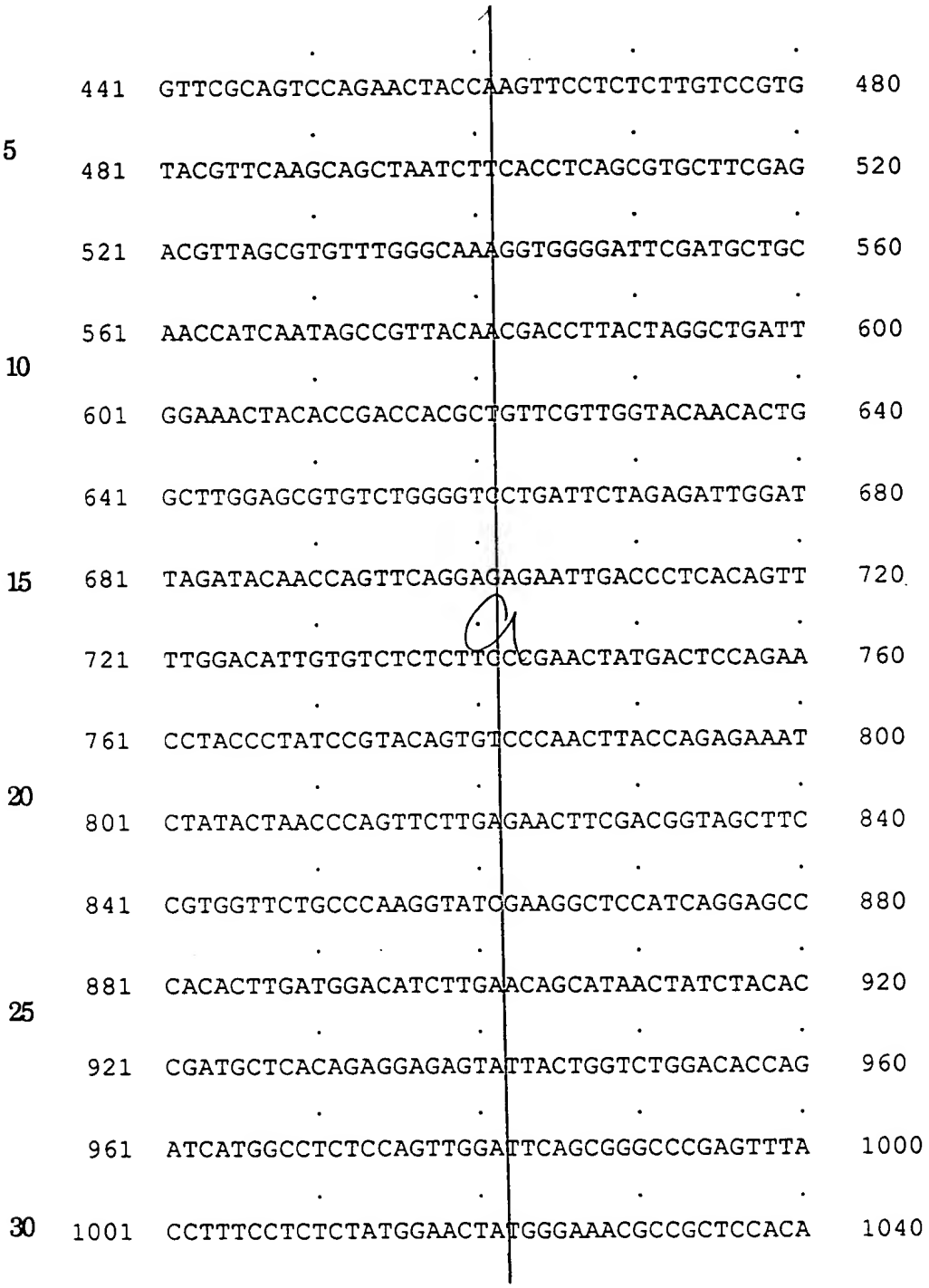
441 GTTCGCAGTCCAGAACTACCAAGTTCCTCTCTTGTCCGTG 480
481 TACGTTCAAGCAGCTAATCTTCACCTCAGCGTGCTTCGAG 520
521 ACGTTAGCGTGTTTGGGCAAAGGTGGGGATTCGATGCTGC 560
561 AACCATCAATAGCCGTTACAACGACCTTACTAGGCTGATT 600
601 GGAAACTACACCGACCACGCTGTTCGTTGGTACAACACTG 640
641 GCTTGGAGCGTGTCTGGGGTCCTGATTCTAGAGATTGGAT 680
681 TAGATACAACCAGTTCAGGAGAGAATTGACCCTCACAGTT 720
721 TTGGACATTGTGTCTCTCTTGCCGAACTATGACTCCAGAA 760
761 CCTACCCTATCCGTACAGTGTCCCAACTTACCAGAGAAAT 800
801 CTATACTAACCCAGTTCTTGAGAACTTCGACGGTAGCTTC 840
841 CGTGGTTCTGCCCAAGGTATCGAAGGCTCCATCAGGAGCC 880
881 CACACTTGATGGACATCTTGAACAGCATAACTATCTACAC 920
921 CGATGCTCACAGAGGAGAGTATTACTGGTCTGGACACCAG 960
961 ATCATGGCCTCTCCAGTTGGATTCAGCGGGCCCGAGTTTA 1000
1001 CCTTTCCTCTCTATGGAACTATGGGAAACGCCGCTCCACA 1040

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1041  ACAACGTATCGTTGCTCAACTAGGTCAGGGTGTCTACAGA  1080
1081  ACCTTGTCTTCCACCTTGTACAGAAGACCCTTCAATATCG  1120
1121  GTATCAACAACCAGCAACTTTCCGTTCTTGACGGAACAGA  1160
1161  GTTCGCCTATGGAACCTCTTCTAACTTGCCATCCGCTGTT  1200
1201  TACAGAAAGAGCGGAACCGTTGATTCCTTGGACGAAATCC  1240
1241  CACCACAGAACAACAATGTGCCACCCAGGCAAGGATTCTC  1280
1281  CCACAGGTTGAGCCACGTGTCCATGTTCCGTTCCGGATTC  1320
1321  AGCAACAGTTCCGTGAGCATCATCAGAGCTCCTATGTTCT  1360
1361  CATGGATTCATCGTAGTGCTGAGTTCAACAATATCATTCC  1400
1401  TTCCTCTCAAATCACCCAAATCCCATTGACCAAGTCTACT  1440
1441  AACCTTGGATCTGGAACTTCTGTCGTGAAAGGACCAGGCT  1480
1481  TCACAGGAGGTGATATTCTTAGAAGAACTTCTCCTGGCCA  1520
1521  GATTAGCACCCTCAGAGTTAACATCACTGCACCACTTTCT  1560
1561  CAAAGATATCGTGTCAGGATTCGTTACGCATCTACCACTA  1600
1601  ACTTGCAATTCCACACCTCCATCGACGGAAGGCCTATCAA  1640
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1641  TCAGGGTAACTTCTCCGCAACCATGTCAAGCGGCAGCAAC  1680
1681  TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTC  1720
1721  CTTTCAACTTCTCTAACGGATCAAGCGTTTTCACCCTTAG  1760
1761  CGCTCATGTGTTCAATTCTGGCAATGAAGTGTACATTGAC  1800
1801  CGTATTGAGTTTGTGCCTGCCGAAGTTACCCTCGAGGCTG  1840
1841  AGTACAACCTTGAGAGAGCCCAGAAGGCTGTGAACGCCCT  1880
1881  CTTTACCTCCACCAATCAGCTTGGCTTGAAAACTAACGTT  1920
1921  ACTGACTATCACATTGACCAAGTGTCCAACTTGGTCACCT  1960
1961  ACCTTAGCGATGAGTTCTGCCTCGACGAGAAGCGTGAACT  2000
2001  CTCCGAGAAAGTTAAACACGCCAAGCGTCTCAGCGACGAG  2040
2041  AGGAATCTCTTGCAAGACTCCAACTTCAAAGACATCAACA  2080
2081  GGCAGCCAGAACGTGGTTGGGGTGGAAGCACCGGGATCAC  2120
2121  CATCCAAGGAGGCGACGATGTGTTCAAGGAGAACTACGTC  2160
2161  ACCCTCTCCGGAACTTTCGACGAGTGCTACCCTACCTACT  2200
2201  TGTACCAGAAGATCGATGAGTCCAAACTCAAAGCCTTCAC  2240
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2241  CAGGTATCAACTTAGAGGCTACATCGAAGACAGCCAAGAC  2280
2281  CTTGAAATCTACTCGATCAGGTACAATGCCAAGCACGAGA  2320
2321  CCGTGAATGTCCCAGGTACTGGTTCCCTCTGGCCACTTTC  2360
2361  TGCCCAATCTCCCATTGGGAAGTGTGGAGAGCCTAACAGA  2400
2401  TGCGCTCCACACCTTGAGTGGAATCCTGACTTGGACTGCT  2440
2441  CCTGCAGGGATGGCGAGAAGTGTGCCCACCATTCTCATCA  2480
2481  CTTCTCCTTGGACATCGATGTGGGATGTACTGACCTGAAT  2520
2521  GAGGACCTCGGAGTCTGGGTCATCTTCAAGATCAAGACCC  2560
2561  AAGACGGACACGCAAGACTTGGCAACCTTGAGTTTCTCGA  2600
2601  AGAGAAACCATTGGTCGGTGAAGCTCTCGCTCGTGTGAAG  2640
2641  AGAGCAGAGAAGAAGTGGAGGGACAAACGTGAGAAACTCG  2680
2681  AATGGGAAACTAACATCGTTTACAAGGAGGCCAAAGAGTC  2720
2721  CGTGGATGCTTTGTTCGTGAACTCCCAATATGATCAGTTG  2760
2761  CAAGCCGACACCAACATCGCCATGATCCACGCCGCAGACA  2800
2801  AACGTGTGCACAGCATTCGTGAGGCTTACTTGCCTGAGTT  2840
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2841 GTCCGTGATCCCTGGTGTGAACGCTGCCATCTTCGAGGAA 2880
2881 CTTGAGGGACGTATCTTTACCGCATTCTCCTTGTACGATG 2920
2921 CCAGAAACGTCATCAAGAACGGTGACTTCAACAATGGCCT 2960
2961 CAGCTGCTGGAATGTGAAAGGTCATGTGGACGTGGAGGAA 3000
3001 CAGAACAATCAGCGTTCCGTCCTGGTTGTGCCTGAGTGGG 3040
3041 AAGCTGAAGTGTCCCAAGAGGTTAGAGTCTGTCCAGGTAG 3080
3081 AGGCTACATTCTCCGTGTGACCGCTTACAAGGAGGGATAC 3120
3121 GGTGAGGGTTGCGTGACCATCCACGAGATCGAGAACAACA 3160
3161 CCGACGAGCTTAAGTTCTCCAACTGCGTCGAGGAAGAAAT 3200
3201 CTATCCCAACAACACCGTTACTTGCAACGACTACACTGTG 3240
3241 AATCAGGAAGAGTACGGAGGTGCCTACACTAGCCGTAACA 3280
3281 GAGGTTACAACGAAGCTCCTTCCGTTCCTGCTGACTATGC 3320
3321 CTCCGTGTACGAGGAGAAATCCTACACAGATGGCAGACGT 3360
3361 GAGAACCCTTGCGAGTTCAACAGAGGTTACAGGGACTACA 3400
3401 CACCACTTCCAGTTGGCTATGTTACCAAGGAGCTTGAGTA 3440
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3441 CTTTCCTGAGACCGACAAAGTGTGGATCGAGATCGGTGAA 3480

3481 ACCGAGGGAACCTTCATCGTGGACAGCGTGGAGCTTCTCT 3520

3521 TGATGGAGGAA 3531

27. A method of Claim 4 further comprising removal of sequences comprising more than five consecutive A+T or G+C bases.

28. A structural gene sequence of Claim 13 comprising a majority of plant preferred codons.

29. A structural gene encoding the coat protein of potato leaf roll virus, said gene having the sequence:

1 ATGAGTACTGTCGTGGTTAAGGGAAACGTGAACGGTGGTG 40

41 TTCAACAACCTAGAAGGAGAAGAAGGCAATCCCTTCGTAG 80

81 GAGAGCTAACAGAGTTCAGCCAGTGGTTATGGTCACTGCT 120

121 CCTGGGCAACCAAGAAGGAGAAGAAGGAGAAGAGGAGGTA 160

161 ATCGCAGATCAAGAAGAACTGGAGTTCCCAGAGGAAGAGG 200

201 TTCAAGCGAGACATTCGTGTTTACAAAGGACAACCTCGTG 240

241 GGCAACTCCCAAGGAAGTTTCACCTTCGGACCAAGTGTTT 280

281 CAGACTGTCCAGCATTCAAGGATGGAATACTCAAGGCTTA 320

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321  CCATGAGTACAAGATCACAAGTATCTTGCTTCAGTTCGTC  360
361  AGCGAGGCCTCTTCCACCTCTCCAGGCTCCATCGCTTATG  400
401  AGTTAGATCCACATTGCAAAGTTTCATCCCTCCAGTCCTA  440
441  CGTCAACAAGTTCCAAATCACAAAGGGTGGTGCTAAGACC  480
481  TATCAAGCTCGTATGATCAACGGAGTTGAATGGCACGATT  520
521  CTTCTGAGGATCAGTGCAGAATCCTTTGGAAAGGAAATGG  560
561  AAAGTCTTCAGATCCAGCTGGATCTTTCAGAGTTACCATC  600
601  AGAGTTGCTCTTCAAAACCGAAAG  624.
```

30. A chimeric plant gene which comprises a structural coding sequence encoding an insecticidal protein of *Bacillus thuringiensis*, said structural coding sequence being modified to reduce the number of putative polyadenylation signals within said structural coding sequence.

31. A chimeric plant gene of Claim 30 in which the polyadenylation signals are selected from the group consisting of AATAAA, AATAAT, AACCAA, ATATAA, AATCAA, ATACTA, ATAAAA, ATGAAA, AAGCAT, ATTAAT, ATACAT, AAAATA, ATTAAA, AATTAA, AATACA and CATAAA.

32. A chimeric plant gene of Claim 31 in which said structural coding sequence is further modified to reduce the number of ATTTA sequences within said structural coding sequence.

33. A chimeric plant gene of Claim 32 in which said structural coding sequence is substantially devoid of polyadenylation signals and ATTTA sequences.

34. A transformed plant cell containing a gene of Claim 33.

35. A transformed plant cell of Claim 34 selected from the group consisting of soybean, cotton, alfalfa, oilseed rape, flax, tomato, sugarbeet, sunflower, potato, tobacco, maize, rice and wheat.

36. A plant comprising transformed plant cells of Claim 34.

37. A plant of Claim 36 which comprises plant cells of Claim 35.

38. A seed produced by a plant of Claim 36.